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PCRRDSP TTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPS QNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLALRVARMPGLERSVRERFLPVH

Fig. 1

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GCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC
GCGCACGCTGGTTTTCTGCTTGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
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AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCCTGGCC
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GGCTGGGGTCCGACACCAAGGGCGGGCCGCGGGCCTTGACAGCTGAAGCTGCGTCGGCGG
CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCAGGCTGCTGCAGGCGCTG
CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC
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CTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

6322560

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNNG
GGAGCGTGACGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCAAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

Fig. 3

SEQ ID No: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID No: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID No: 6 1
 SEQ ID No: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 G
 SEQ ID No: 4 178 CA-TTCTGGAACCTACCTGGAGCGC
 SEQ ID No: 5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNNG
 SEQ ID No: 6 2 CAGTTCTGGAACCTACCTGGAGCNCCTGCCGCTACTGCAACGTCCTCTGCGG
 SEQ ID No: 3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNNG
 SEQ ID No: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGGCCT
 SEQ ID No: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
 SEQ ID No: 7 1 GAGGGCCCCCAGGAGTGGTGGCCGGAGGTG
 SEQ ID No: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
 SEQ ID No: 5 151 GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNTTCTGTGCTTGGAGCAC
 SEQ ID No: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGTGCTTGGAGCAC
 SEQ ID No: 7 32 TGGCAGGGGTACAGTTGCTGGTCCCGCAGCCTTGACCCCTGAGCTAGGACAC
 SEQ ID No: 3 151 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGTGCTTGGAGCAC
 SEQ ID No: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGNCNCGGGCACCCCCAGCCA
 SEQ ID No: 6 152 GCATCGTGTCCACCTGGTGNCGGCGTGATTNCCCGGGCACCCCCAGCCA
 SEQ ID No: 7 82 CAGTTCCCTGACCCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
 SEQ ID No: 8 1 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCCCCGGGCACCCCCAGCCA
 SEQ ID No: 10 1 CTTGTCCACCTGGTGNCGGCGTGATTNCCC-GGGCACCCCCAGCCA
 SEQ ID No: 3 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCCCCGGGCACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA - TGCAAAAGCCGTG
 SEQ ID NO: 7 132 GAACACGAGN - CC - AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 8 51 GAACACGAG - GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 10 47 GAACACGAGTGC - AGCCT - CCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT
 SEQ ID NO: 3 251 GAACACGAGTGCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
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 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
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 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 10 247 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 9 186 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
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Fig. 4 (cont.)

UNA 30942
H1NFR2

MRALCEPGLISLLGLVIALPALLPVPAVRGVATIPITYPWRD AEIG
MAPVAVWALAVGLELWAAAHALPAQVAFPPYAPLPGSTCRLREYYDOI

DNA 30942
H1NFR2

CRD1
15 ERLVCAQCPPGTFVORPCRRDSPITCGPCPPRH YTOFWNYLERCRYCNVL
25 AOMCCSKCSPGQNAKVFCITKTS DITVCDSCGEOSTYTQIWNWVPECLSCGSR

DNA 30942
H1NFR2

CRD2
75 CGEREEEARACHATHNRACRCRTGFF...AHAG...FCLHASCPPGAGV
100 CSSDOVETOACTREQNRICTCRPGWYCALSKOEGCRLCAPLRKCRPGFGV

DNA 30942
H1NFR2

CRD3
139 IAPGTPSONTCQPCPPGTFSSASSSSEQCOPHRNCTALGLALNVPGSSS
150 ARPGETETSDVCKPCA PGTFSSNTTSSSTDCRPHQICNVVA...IPGNAS

DNA 30942
H1NFR2

CRD4
189 HDTLCTSTCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLORLLOALEA
196 RDAVCTSTS...PTRSMAPGAVHLPQPVSTRSQHTOPTPEPSTAPSTSFL

DNA 30942
H1NFR2

229 PEGWGPTP...RAGRAALOLKLRRRLTELGAODGALLVRLLOALRVAMP
241 PMGPSPPAEGSTGDFALPVGLIVGVTA LGLLIIGVVNCVIMTQVKKKPL

DNA 30942
H1NFR2

287 GLERSVRRERFLPVH
293 CLQREAKVPHLPADKARGTQGPEQOHLITAPSSSSSSLESSASALD-RRA

H1NFR2

343 PTRNOPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD

H1NFR2

393 HSSQCSSQASSTMGDTDSSPSES PKDEQVPFSKEECAFRSOLETPETLLG

H1NFR2

443 STEEKPLPLGVPOAGMKPS

Fig. 5

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P - - - - - 25

CRD1

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62
 OPG 26 - - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93
 OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD2

DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4

DcR3 156 G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S 186
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

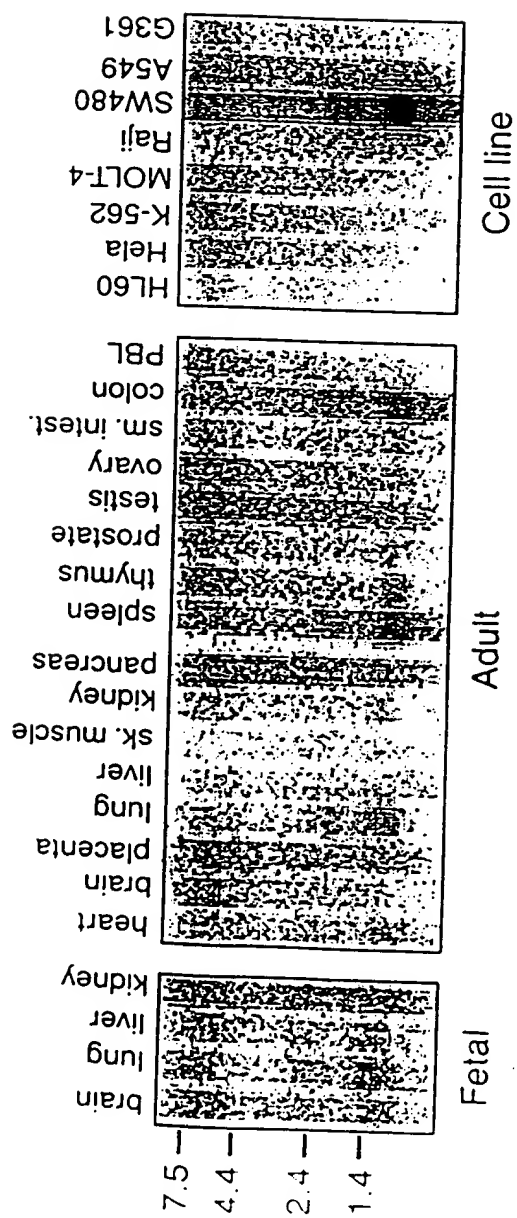


Fig. 7

333T60"03243T60

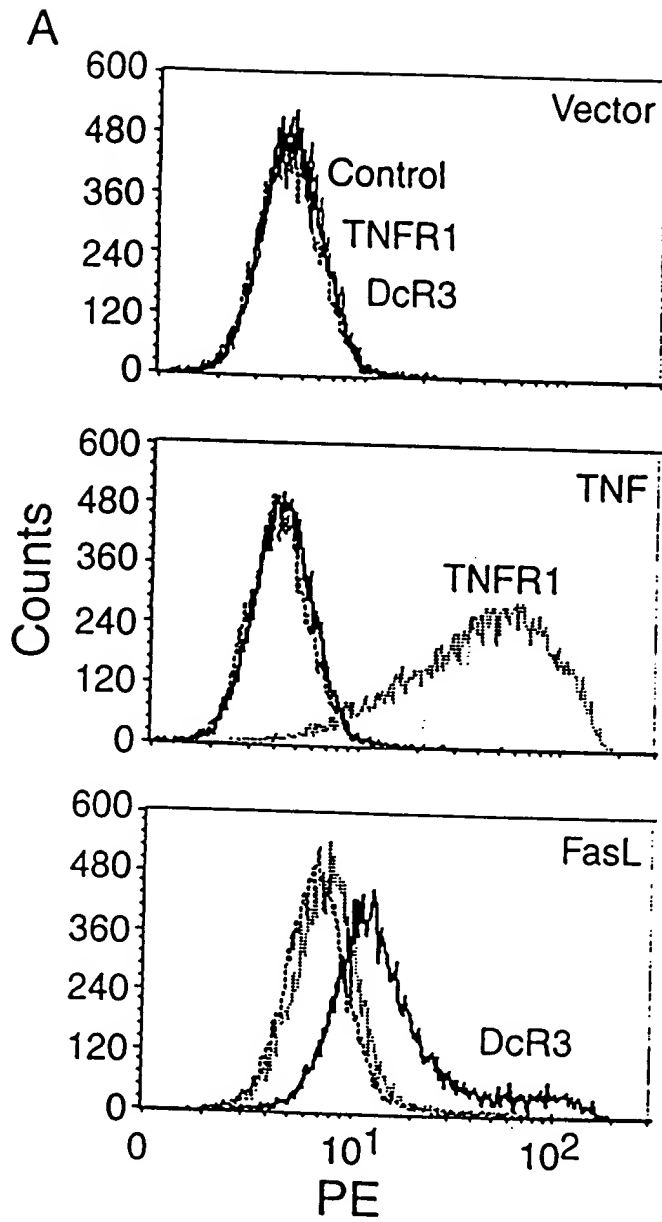
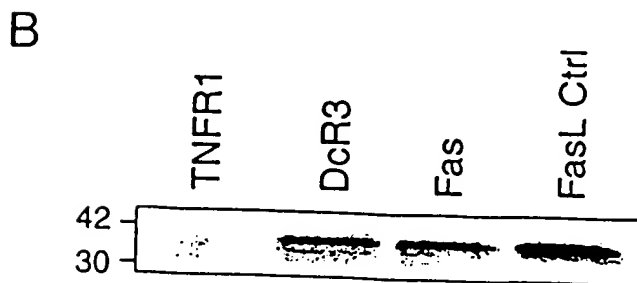


Fig. 8



663760-664370

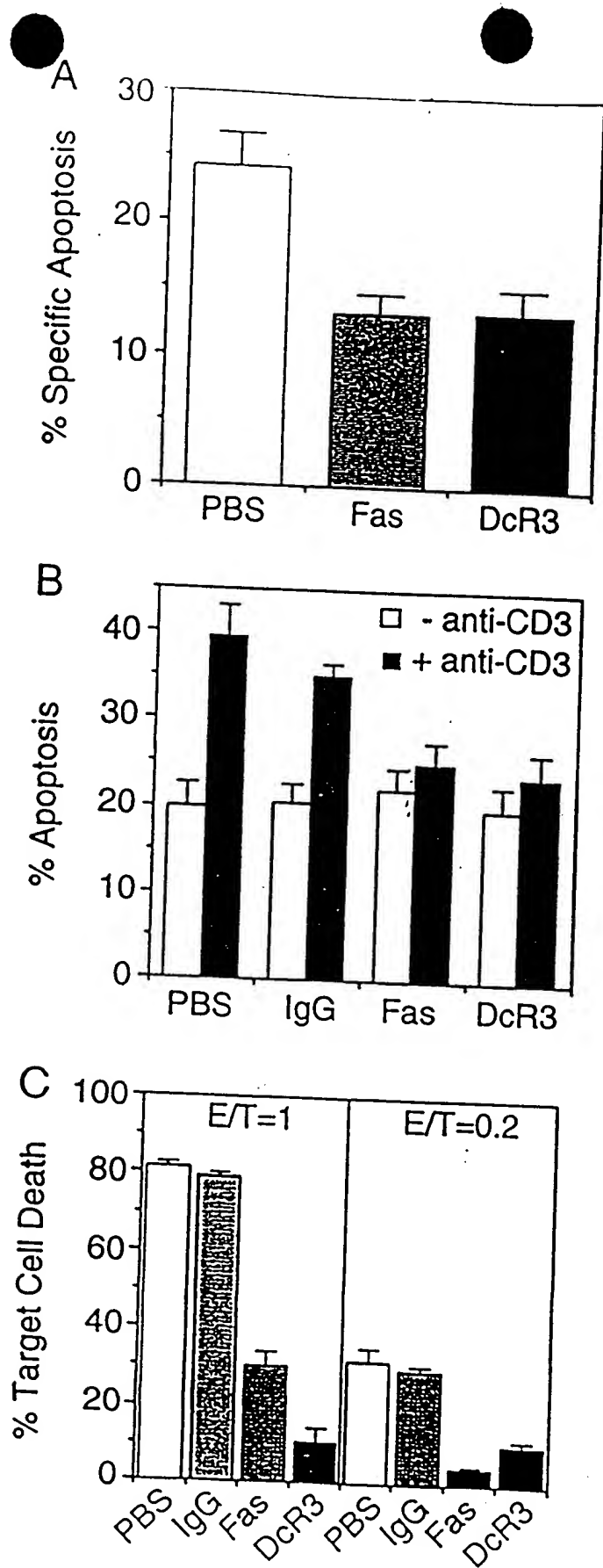


Fig. 9

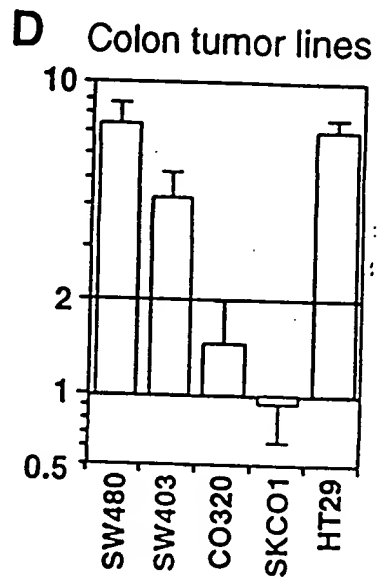
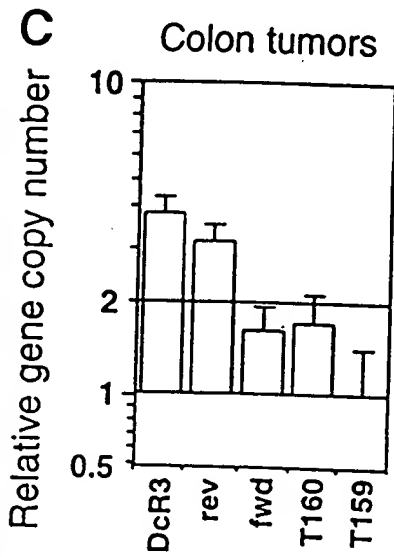
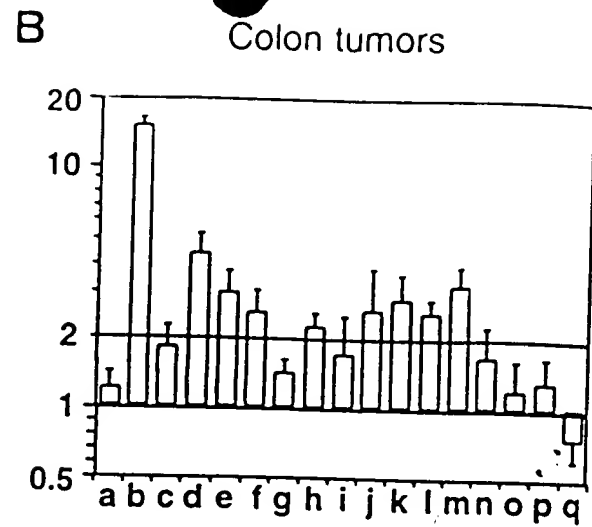
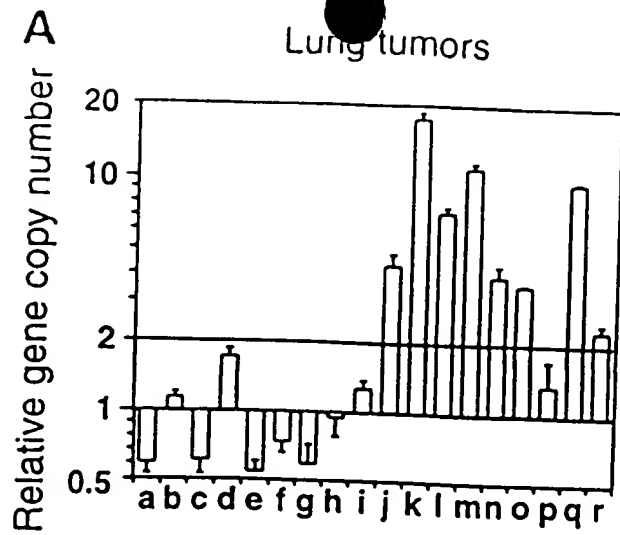


Fig. 10

FIGURE 12

<u>mAb</u>	<u>Isotype</u>	<u>Antigen Specificity (ELISA)</u>					% Blocking (ELISA)
		<u>DcR3</u>	<u>DR4</u>	<u>DR5</u>	<u>DcR1</u>	<u>OPG</u>	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

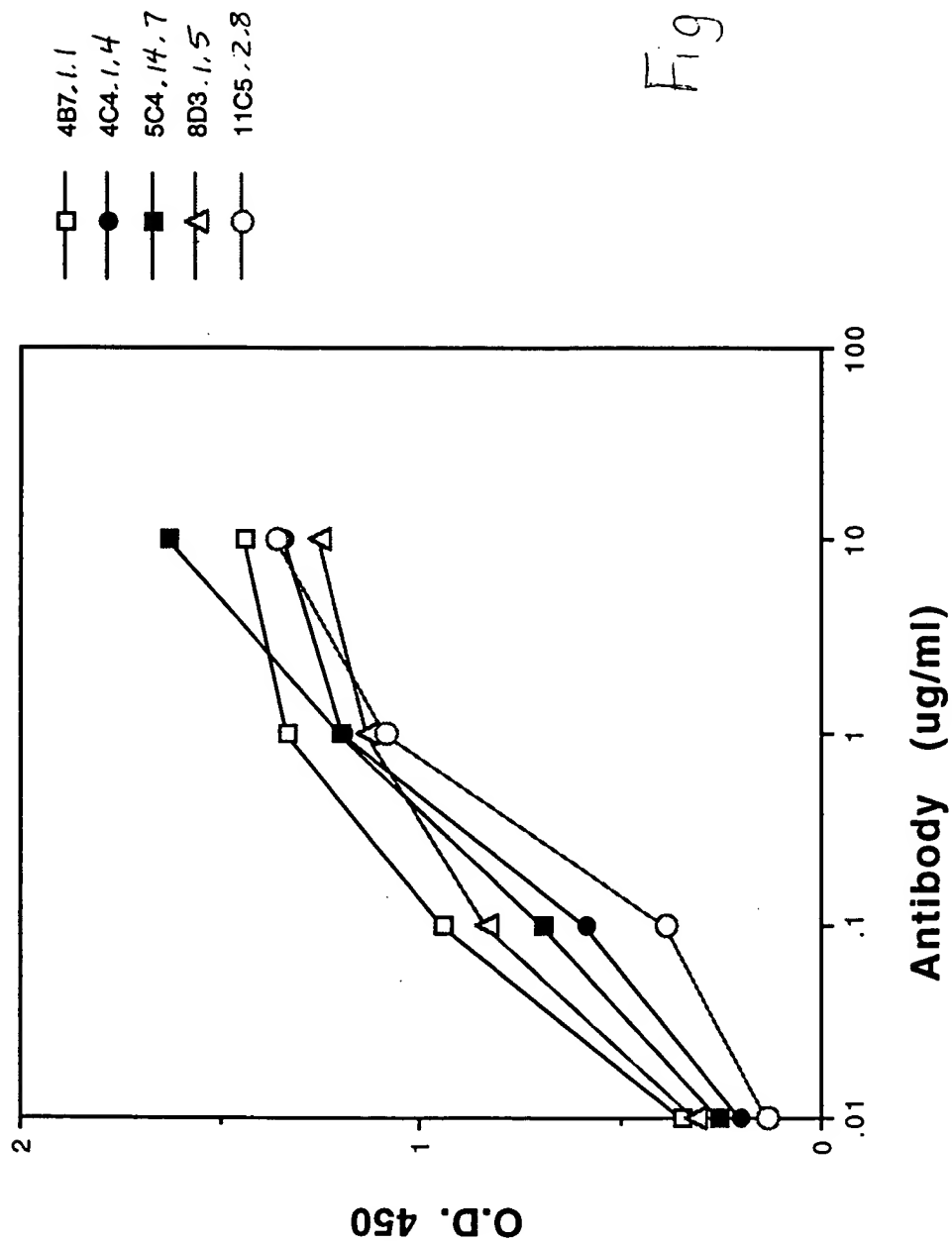


Fig. 13

Fig. 14

